

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Gruys, Kenneth J.

Mitsky, Timothy A.

Kishore, Ganesh M.

Slater, Steven C.

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Padgett, Stephen R.

Stark, David M.

Hinchee, Maud A. W.

Clemente, Thomas E.

Connor-Ward, Dannette V.

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Fedele, Mary J.

Fry, Joyce E.

Howe, Arlene R.

Rozman, Renee J.

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(ii) TITLE OF INVENTION: Methods of Optimizing Substrate Pools and
Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerate
in Bacteria and Plants

(iii) NUMBER OF SEQUENCES: 11

25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB

(B) STREET: 800 North Lindbergh Boulevard

(C) CITY: St. Louis

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(D) STATE: Missouri

(E) COUNTRY: USA

(F) ZIP: 63167

(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 13-MAR-1996

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bond, Gary

(B) REGISTRATION NUMBER: 29,283

(C) REFERENCE/DOCKET NUMBER: 38-21(13585)A

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (314)694-3412

(B) TELEFAX: (314)695-5435

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

35

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG

60

CTGCGCGCGC CGGTTTACGA GCGGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG

120

	TCGTCGCGTC	TTGATAACGT	CATTCTGGTG	AAGCGCGAAG	ATCGCCAGCC	AGTGCACAGC	180
	TTTAAGCTGC	GCGGCGCATA	CGCCATGATG	GCGGGCCTGA	CGGAAGAACA	GAAAGCGCAC	240
5	GGCGTGATCA	CTGCTTCTGC	GGGTAACCAC	GCGCAGGGCG	TCGCGTTTTC	TTCTGCGCGG	300
	TTAGGCGTGA	AGGCCCTGAT	CGTTATGCCA	ACCGCCACCG	CCGACATCAA	AGTCGACCGG	360
10	CTGCGCGGCT	TCGGCGGCGA	AGTGCTGCTC	CACGGCGCGA	ACTTTGATGA	AGCGAAACGC	420
	AAAGCGATCG	AACTGTCACA	GCAGCAGGGG	TTCACCTGGG	TGCCGCCGTT	CGACCATCCG	480
	ATGGTGATTG	CCGGGCAAGG	CACGCTGGCG	CTGGAAGTGC	TCCAGCAGGA	CGCCCATCTC	540
15	GACCGCGTAT	TTGTGCCAGT	CGGCGGCGGC	GGTCTGGCTG	CTTGCGTGGC	GGTGCTGATC	600
	AAACAACTGA	TGCCGCAAAT	CAAAGTGATC	GCCGTAGAAG	CGGAAGACTC	CGCCTGCCTG	660
20	AAAGCAGCGC	TGGATGCGGG	TCATCCGGTT	GATCTGCCGC	GCGTAGGGCT	ATTTGCTGAA	720
	GGCGTAGCGG	TAAAACGCAT	CGGTGACGAA	ACCTTCCGTT	TATGCCAGGA	GATCTCGAC	780
	GACATCATCA	CCGTCGATAG	CGATGCGATC	TGTGCGGCGA	TGAAGGATTT	ATTCTGAAGAT	840
25	GTGCGCGCGG	TGGCGGAACC	CTCTGGCGCG	CTGGCGCTGG	CGGGAATGAA	AAAATATATC	900
	GCCCTGCACA	ACATTGCGGG	CGAACGGCTG	GCGCATATTC	TTTCCGGTGC	CAACGTGAAC	960
30	TTCCACGGCC	TGCGCTACGT	CTCAGAACGC	TGCGAACTGG	TCGAACAGCG	TGAAGCGTTG	1020
	TTGGCGGTGA	CCATTCCGGA	AGAAAAAGGC	AGCTTCCTCA	AATTCTGCCA	ACTGCTTGGC	1080
	GGGCGTTCCG	TCACCGAGTT	CAACTACCGT	TTTGCCGATG	CCAAAAACGC	CTGCATCTTT	1140
35	GTCGGTGTGC	GCCTGAGCCG	CGGCCTCGAA	GAGCGCAAAG	AAATTTTGCA	GATGCTCAAC	1200
	GACGGCGGCT	ACAGCGTGGT	TGATCTCTCC	GACGACGAAA	TGGCGAAGCT	ACACGTGCGC	1260

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320

CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

5

TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GGCGTTCGAA 1440

CTTGCGCACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

10 GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTTTTGGATC CGATATCTTA ACCCGCCAAA AAGAACCTGA ACGCCG 46

30 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTGGATC CATGGCTGAC TCGCAACCCC TGTCGG

37

10 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs

(B) TYPE: nucleic acid

15

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "synthetic DNA"

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25

CAGCTTCGAG TTCCCGGAAT CACCGGGCGC GTTCCTGCGC TTCC

44

(2) INFORMATION FOR SEQ ID NO:5:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: .

5 ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG 120

TCGTGCGGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

10 TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300

15 TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

20 ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

25 AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

GGCGTAGCGG TAAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780

30 GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840

GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900

35 GCCCTGCACA ACATTGCGCG CGAACGGCTG GCGCATATTC TTCCGGTGTC CAACGTGAAC 960

TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

GGGCGTTTCG TCACCGAGTT CAACTACCGT TTTGCCGATG CAAAAACGC CTGCATCTTT 1140

5 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAGTTC 1320

10 CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

TCTTTGTTCC ACTATCGCAG CCATGGCACC GACTACGGGC GCGTACTGGC GCGGTTTCGAA 1440

15 CTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

- (2) INFORMATION FOR SEQ ID NO:6:
- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: other nucleic acid
- (A) DESCRIPTION: /desc = "synthetic DNA"

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

35 TATCGCAGCC ACGGCACCGA CTACGGGCGC GTACTGGCGG CGTTCGAATT TGGCGACCAT 60

GAACC 65

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1545 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

15

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAAACTG 120

20

TCGTGCGGTC TTGATAACGT CATTCTGGTG AAGCGGAAG ATCGCCAGCC AGTGACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300

25

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

30

AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

35

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

GGCGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780
GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840
5 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900
GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTTCCGGTGC CAACGTGAAC 960
10 TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020
TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080
GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140
15 GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200
GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260
20 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTCGAATTC 1320
CCGGAATCAC CGGGCGCGCT GCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380
TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGC GTTCGAA 1440
25 TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500
GACGAAACCA ATAACCCGGC GTTCAGGTTT TTTTGGCGG GTTAA 1545

30 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCTGACT CGCAACCCCT GTCCGGTGCT CCGGAAGGTG CCGAATATTT AAGAGCAGTG 60

CTGCGCGCGC CGGTTTACGA GGCGGCGCAG GTTACGCCGC TACAAAAAAT GGAAAACTG 120

10 TCGTCGCGTC TTGATAACGT CATTCTGGTG AAGCGCGAAG ATCGCCAGCC AGTGCACAGC 180

TTTAAGCTGC GCGGCGCATA CGCCATGATG GCGGGCCTGA CGGAAGAACA GAAAGCGCAC 240

15 GGCGTGATCA CTGCTTCTGC GGGTAACCAC GCGCAGGGCG TCGCGTTTTT TTCTGCGCGG 300

TTAGGCGTGA AGGCCCTGAT CGTTATGCCA ACCGCCACCG CCGACATCAA AGTCGACCGG 360

CTGCGCGGCT TCGGCGGCGA AGTGCTGCTC CACGGCGCGA ACTTTGATGA AGCGAAACGC 420

20 AAAGCGATCG AACTGTCACA GCAGCAGGGG TTCACCTGGG TGCCGCCGTT CGACCATCCG 480

ATGGTGATTG CCGGGCAAGG CACGCTGGCG CTGGAAGTGC TCCAGCAGGA CGCCCATCTC 540

25 GACCGCGTAT TTGTGCCAGT CGGCGGCGGC GGTCTGGCTG CTTGCGTGGC GGTGCTGATC 600

AAACAACTGA TGCCGCAAAT CAAAGTGATC GCCGTAGAAG CGGAAGACTC CGCCTGCCTG 660

AAAGCAGCGC TGGATGCGGG TCATCCGGTT GATCTGCCGC GCGTAGGGCT ATTTGCTGAA 720

30 GGCGTAGCGG TAAACGCAT CGGTGACGAA ACCTTCCGTT TATGCCAGGA GTATCTCGAC 780

GACATCATCA CCGTCGATAG CGATGCGATC TGTGCGGCGA TGAAGGATTT ATTCGAAGAT 840

35 GTGCGCGCGG TGGCGGAACC CTCTGGCGCG CTGGCGCTGG CGGGAATGAA AAAATATATC 900

GCCCTGCACA ACATTCGCGG CGAACGGCTG GCGCATATTC TTCCGGTGC CAACGTGAAC 960

TTCCACGGCC TGCCTACGT CTCAGAACGC TCGAACTGG TCGAACAGCG TGAAGCGTTG 1020

TTGGCGGTGA CCATTCCGGA AGAAAAAGGC AGCTTCCTCA AATTCTGCCA ACTGCTTGGC 1080

5 GGGCGTTCGG TCACCGAGTT CAACTACCGT TTTGCCGATG CCAAAAACGC CTGCATCTTT 1140

GTCGGTGTGC GCCTGAGCCG CGGCCTCGAA GAGCGCAAAG AAATTTTGCA GATGCTCAAC 1200

GACGGCGGCT ACAGCGTGGT TGATCTCTCC GACGACGAAA TGGCGAAGCT ACACGTGCGC 1260

10 TATATGGTCG GCGGACGTCC ATCGCATCCG TTGCAGGAAC GCCTCTACAG CTTGAGTTTC 1320

CCGGAATCAC CGGGCGCGTT CCTGCGCTTC CTCAACACGC TGGGTACGTA CTGGAACATT 1380

15 TCTTTGTTCC ACTATCGCAG CCACGGCACC GACTACGGGC GCGTACTGGC GGC GTTCGAA 1440

TTTGGCGACC ATGAACCGGA TTTCGAAACC CGGCTGAATG AGCTGGGCTA CGATTGCCAC 1500

GACGAAACCA ATAACCCGGC GTTCAGGTTC TTTTGGCGG GTTAA 1545

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(2) INFORMATION FOR SEQ ID NO:9:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1185 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: DNA (genomic)

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGACGCGTG AAGTGGTAGT GGTAAGCGGT GTCCGTACCG CGATCGGGAC CTTTGGCGGC 60

AGCCTGAAGG ATGTGGCACC GCGGAGCTG GCGCACTGG TGGTGC GCGA GCGCTGGCG 120
 CGCGCGCAGG TGTCGGGCGA CGATGTCCGC CACGTGGTAT TCGGCAACGT GATCCAGACC 180
 5 GAGCCGCGCG ACATGTATCT GGGCCGCGTC GCGGCCGTCA ACGGCGGGT GACGATCAAC 240
 GCGCCGCGC TGACCGTGAA CCGCCTGTGC GGCTCGGGCC TGCAGGCCAT TGTCAGCGCC 300
 GCGCAGACCA TCCTGCTGGG CGATACCGAC GTCGCCATCG GCGGCGGCGC GGAAAGCATG 360
 10 AGCCGCGCAC CGTACCTGGC GCCGGCAGCG CGCTGGGGCG CACGCATGGG CGACGCCGCG 420
 CTGGTCGACA TGATGTGGG TCGCTGCAC GATCCCTTCC ATCGCATCCA CATGGGCGTG 480
 15 ACCGCCGAGA ATGTCGCCAA GGAATACGAC ATCTCGCGCG CGCAGCAGGA CGAGGCCGCG 540
 CTGGAATCGC ACCGCCGCGC TTCGGCAGCG ATCAAGGCCG GCTACTTCAA GGACCAGATC 600
 GTCCCGGTGG TGAGCAAGGG CCGCAAGGGC GACGTGACCT TCGACACCGA CGAGCACGTG 660
 20 CGCCATGACG CCACCATCGA CGACATGACC AAGCTCAGGC CGGTCTTCGT CAAGGAAAAC 720
 GGCACGGTCA CGGCCGGCAA TGCTCGGGC CTGAACGACG CCGCCGCCGC GGTGGTGATG 780
 25 ATGAGCGCG CCGAAGCCGA GCGCCGCGC CTGAAGCCGC TGGCCGCCT GGTGTCGTAC 840
 GGCCATGCCG GCGTGGACCC GAAGGCCATG GGCATCGGCC CGGTGCCGC GACGAAGATC 900
 GCGCTGGAGC GCGCCGCCCT GCAGGTGTCG GACCTGGACG TGATCGAAGC CAACGAAGCC 960
 30 TTTGCCGCAC AGGCGTGCGC CGTGACCAAG GCGCTCGGTC TGGACCGGC CAAGGTAAAC 1020
 CCGAACGGCT CGGGCATCTC GCTGGGCCAC CCGATCGGCG CCACCGGTGC CCTGATCAG 1080
 35 GTGAAGGCGC TGCATGAGCT GAACGCGCTG CAGGGCCGCT ACGCGCTGGT GACGATGTGC 1140
 ATCGGCGGCG GGCAGGGCAT TGCCGCCATC TTCGAGCGTA TCTGA 1185

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

15

Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:11:

20

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35 Met Thr Arg Glu Val Val Val Val Ser Gly Val Arg Thr Ala Ile Gly
1 5 10 15

Thr Phe Gly Gly Ser Leu Lys Asp Val Ala Pro Ala Glu Leu Gly Ala
20 25 30

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Leu Val Val Arg Glu Ala Leu Ala Arg Ala Gln Val Ser Gly Asp Asp
 35 40 45

5 Val Gly His Val Val Phe Gly Asn Val Ile Gln Thr Glu Pro Arg Asp
 50 55 60

Met Tyr Leu Gly Arg Val Ala Ala Val Asn Gly Gly Val Thr Ile Asn
 65 70 75 80

10 Ala Pro Ala Leu Thr Val Asn Arg Leu Cys Gly Ser Gly Leu Gln Ala
 85 90 95

Ile Val Ser Ala Ala Gln Thr Ile Leu Leu Gly Asp Thr Asp Val Ala
 15 100 105 110

Ile Gly Gly Gly Ala Glu Ser Met Ser Arg Ala Pro Tyr Leu Ala Pro
 115 120 125

20 Ala Ala Arg Trp Gly Ala Arg Met Gly Asp Ala Gly Leu Val Asp Met
 130 135 140

Met Leu Gly Ala Leu His Asp Pro Phe His Arg Ile His Met Gly Val
 145 150 155 160

25 Thr Ala Glu Asn Val Ala Lys Glu Tyr Asp Ile Ser Arg Ala Gln Gln
 165 170 175

Asp Glu Ala Ala Leu Glu Ser His Arg Arg Ala Ser Ala Ala Ile Lys
 30 180 185 190

Ala Gly Tyr Phe Lys Asp Gln Ile Val Pro Val Val Ser Lys Gly Arg
 195 200 205

35 Lys Gly Asp Val Thr Phe Asp Thr Asp Glu His Val Arg His Asp Ala
 210 215 220

Thr Ile Asp Asp Met Thr Lys Leu Arg Pro Val Phe Val Lys Glu Asn

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	225	230	235	240
	Gly Thr Val Thr Ala Gly Asn Ala Ser Gly Leu Asn Asp Ala Ala Ala			
		245	250	255
5	Ala Val Val Met Met Glu Arg Ala Glu Ala Glu Arg Arg Gly Leu Lys			
	260	265	270	
	Pro Leu Ala Arg Leu Val Ser Tyr Gly His Ala Gly Val Asp Pro Lys			
10	275	280	285	
	Ala Met Gly Ile Gly Pro Val Pro Ala Thr Lys Ile Ala Leu Glu Arg			
	290	295	300	
15	Ala Gly Leu Gln Val Ser Asp Leu Asp Val Ile Glu Ala Asn Glu Ala			
	305	310	315	320
	Phe Ala Ala Gln Ala Cys Ala Val Thr Lys Ala Leu Gly Leu Asp Pro			
	325	330	335	
20	Ala Lys Val Asn Pro Asn Gly Ser Gly Ile Ser Leu Gly His Pro Ile			
	340	345	350	
	Gly Ala Thr Gly Ala Leu Ile Thr Val Lys Ala Leu His Glu Leu Asn			
25	355	360	365	
	Arg Val Gln Gly Arg Tyr Ala Leu Val Thr Met Cys Ile Gly Gly Gly			
	370	375	380	
30	Gln Gly Ile Ala Ala Ile Phe Glu Arg Ile			
	385	390		

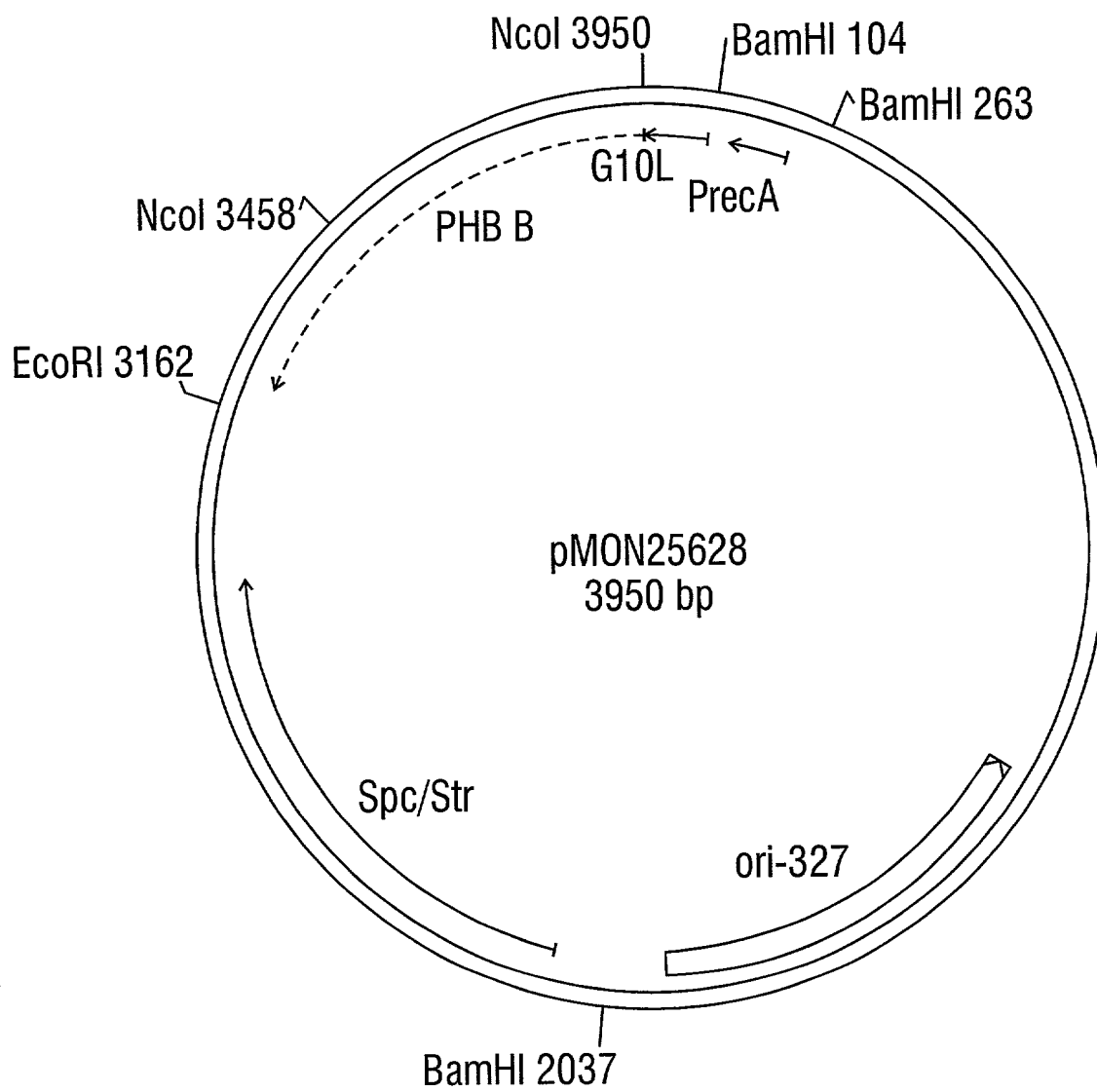


FIG. 18

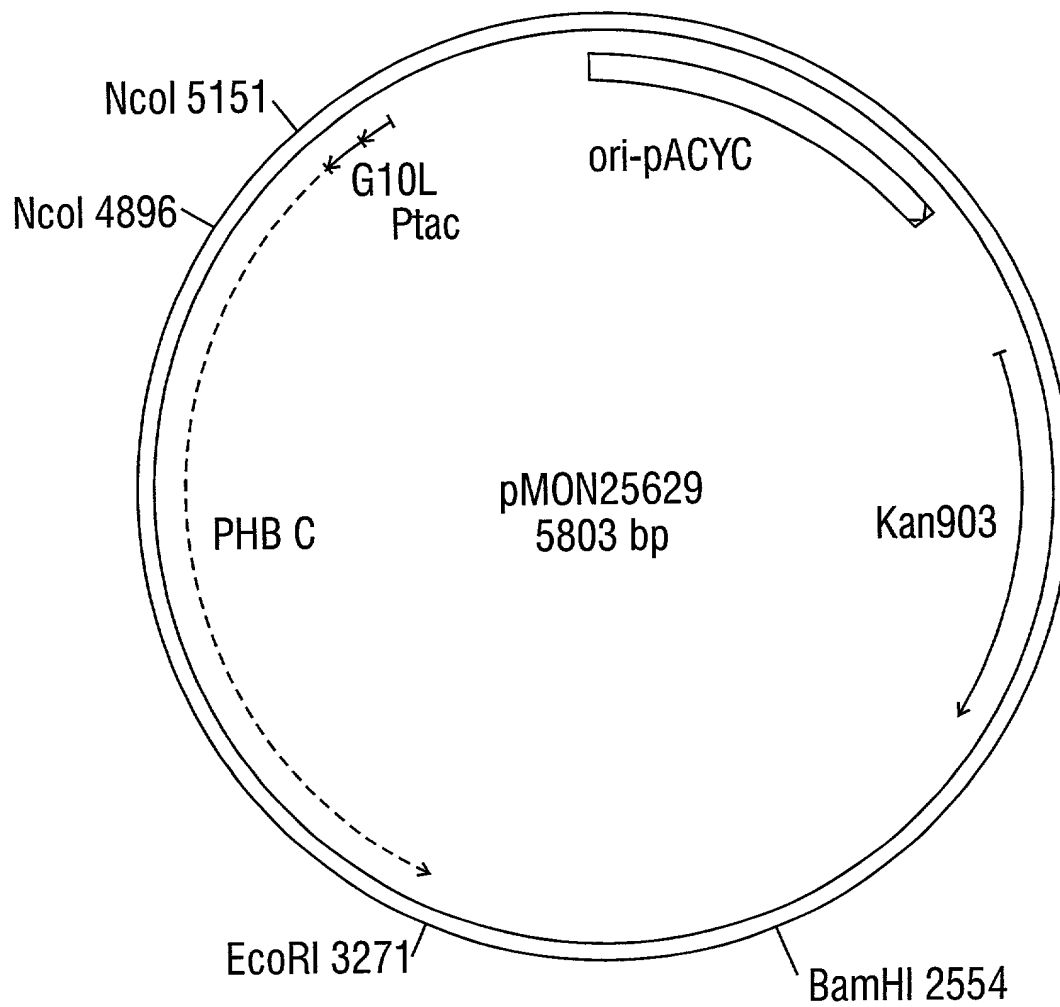


FIG. 19

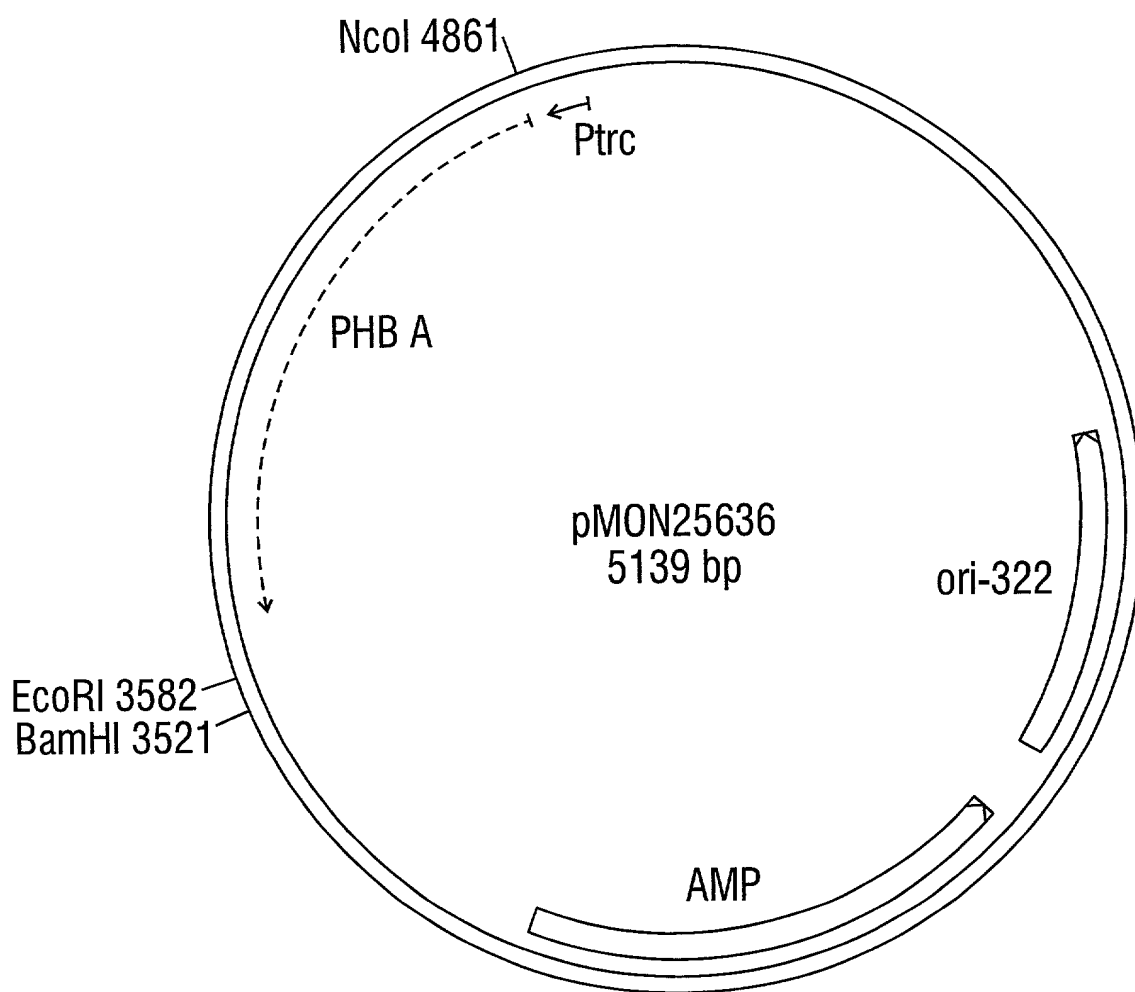


FIG. 20

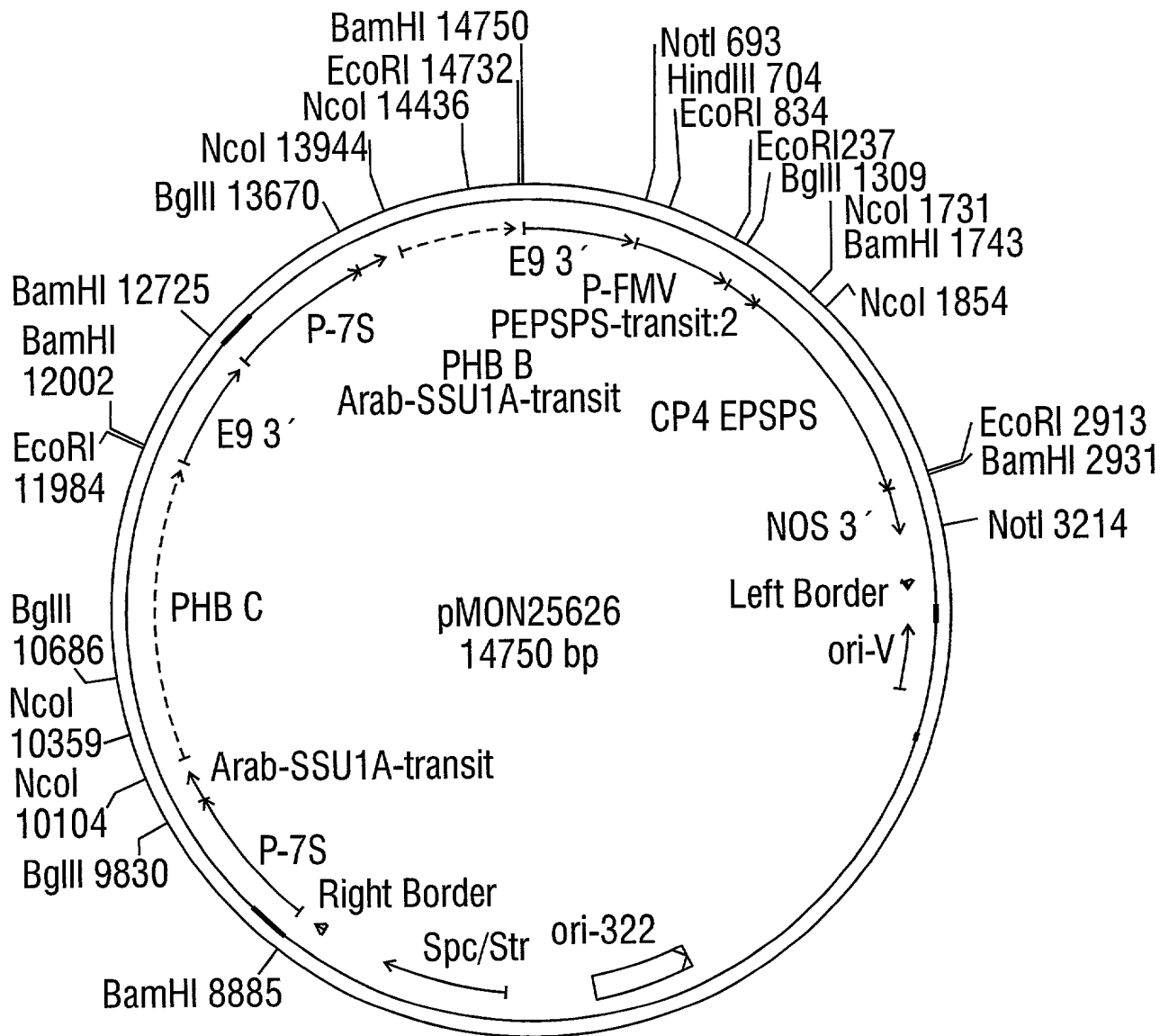


FIG. 21

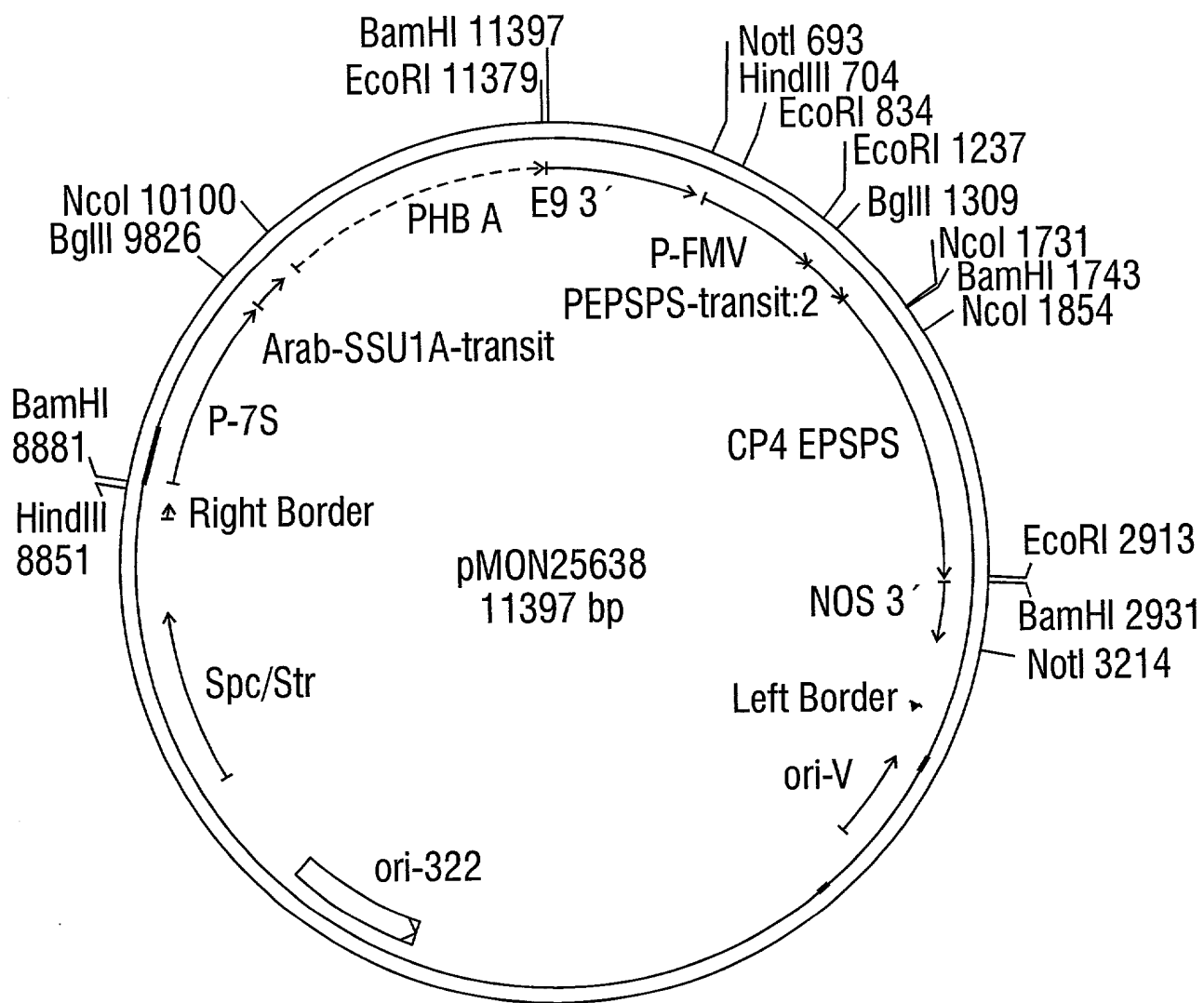


FIG. 22